

1/19

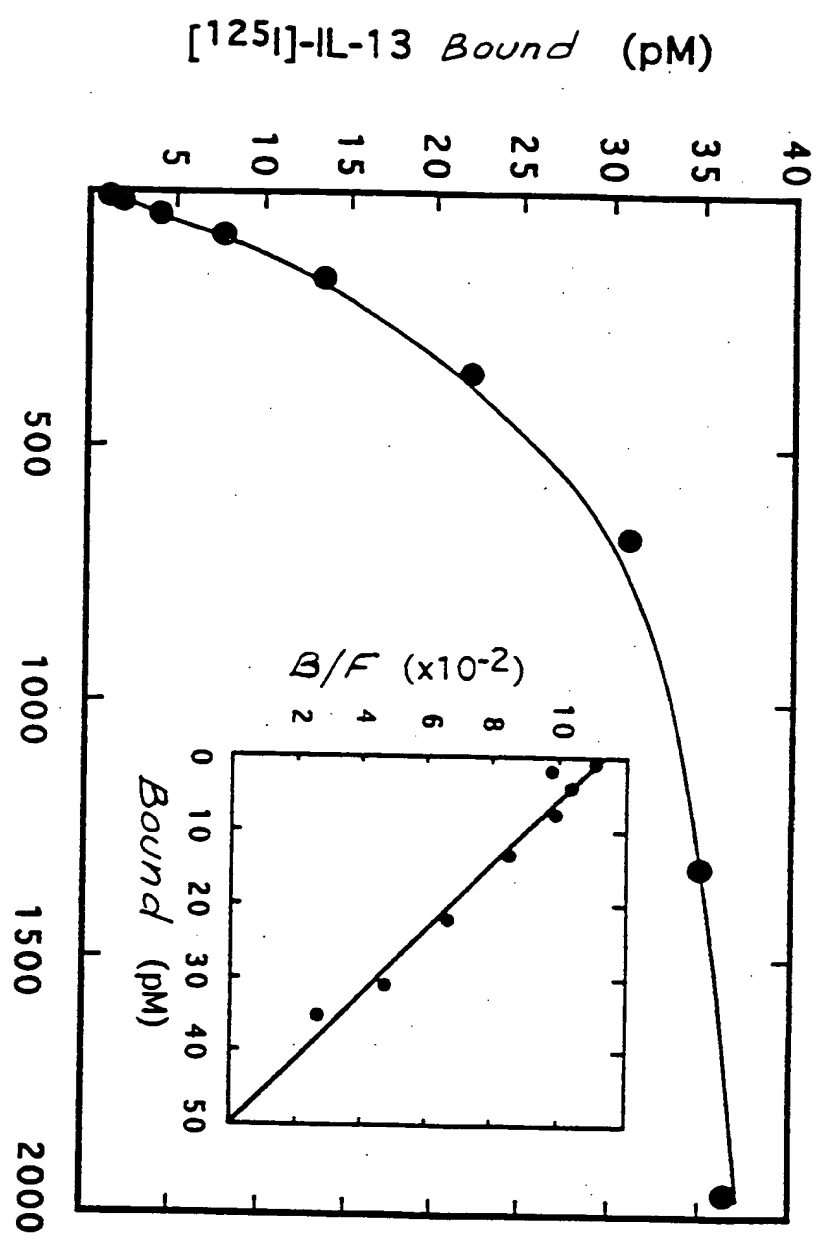
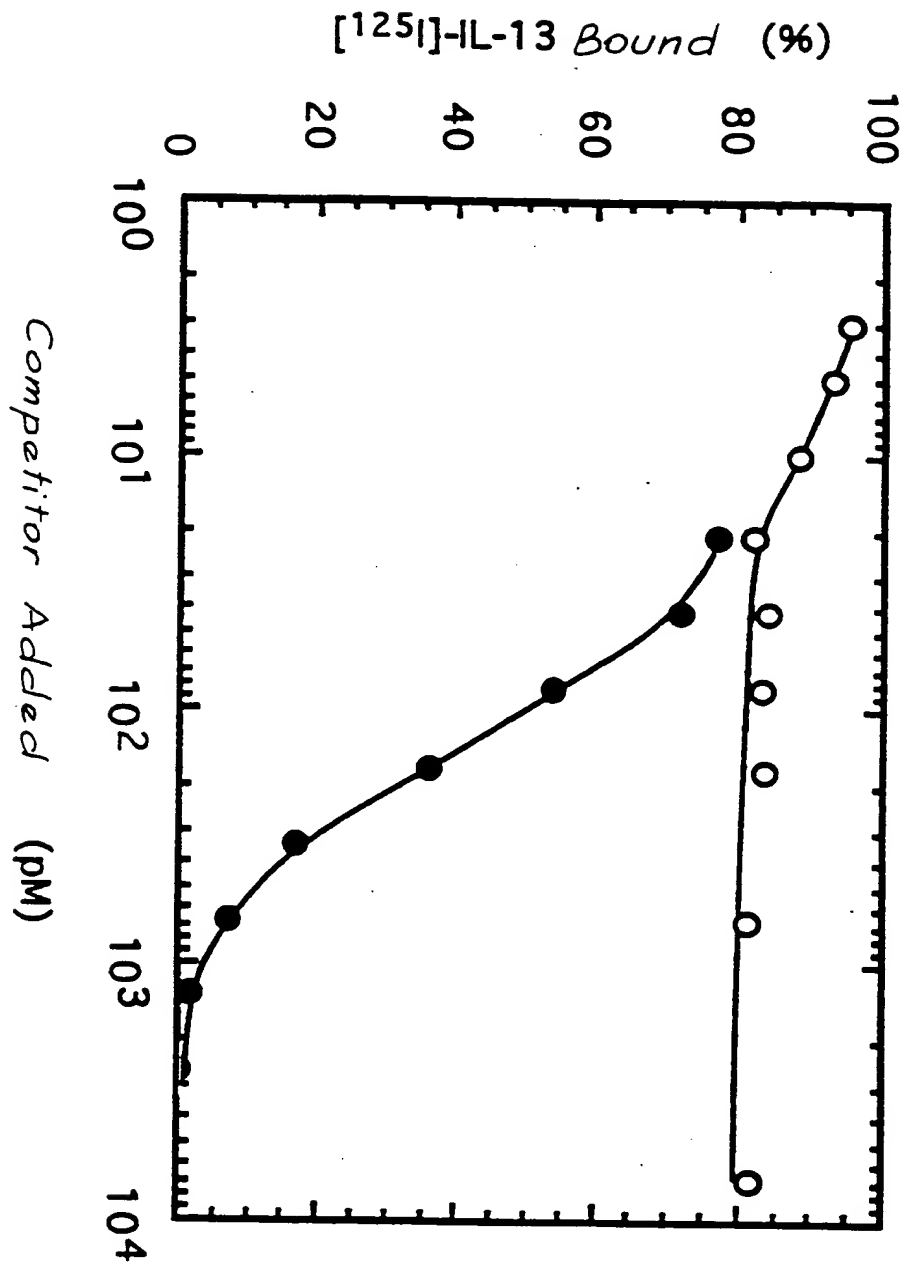


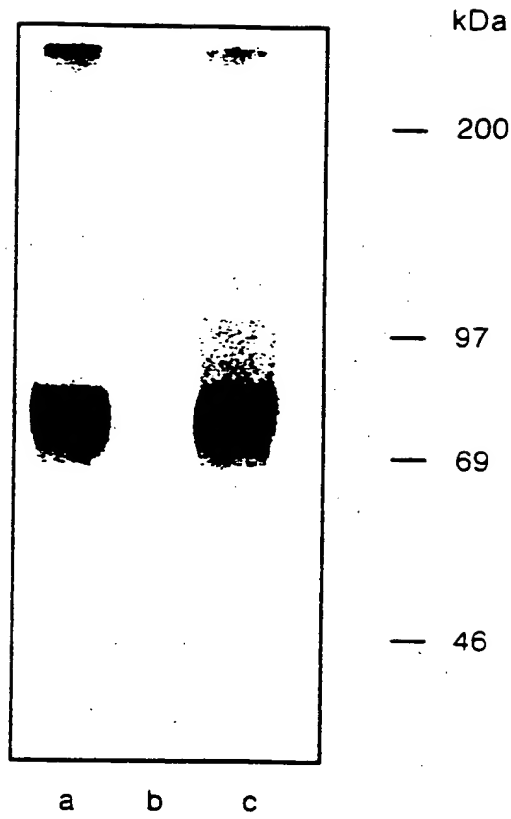
FIG. 1a

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2/19

FIG. 1b

3/19

FIG.1c

09077817-091493

4/19

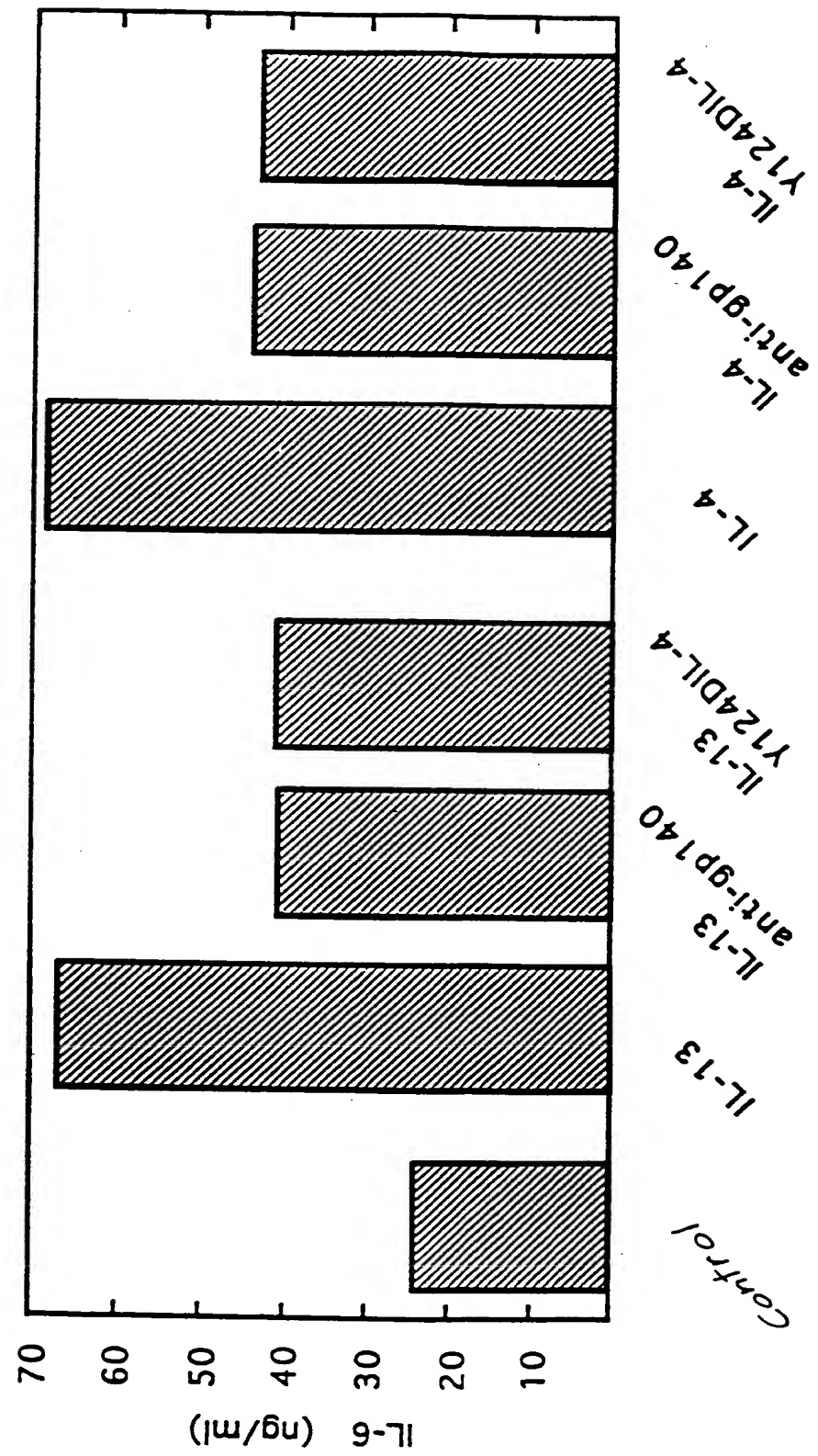


FIG.1d

5/19

1	GGTGCCTGTGCGCGGGGAGAGAGCAATATCAAGGTTTAAATCTCGGAGAAATGGCT	58
1	MetAla	2
59	TTGCTTTGGCTATCGGATGCTTATATACCTTTCTGATAAGCACAAACATTTGGCTGT	118
3	PheValCysLeuAlaIleGlyCysLeuTyrThrPheLeuIleSerThrThrPheGlyCys	22
119	ACTTCATCTTCAGACACCGAGATAAAAGTTAACCTCCTCAGGATTTTGAGATAGTGGAT	178
23	ThrSerSerSerAspThrGluIleLysValAsnProProGlnAspPheGluIleValAsp	42
179	CCCGGATACTTAGGTTATCTCTATTTGGCAATGGCAACCCCTGCTCTGGATCATTTT	238
43	ProGlyTyrLeuGlyTyrLeuTyrLeuGlnTrpGlnProProLeuSerLeuAspHisPhe	62
239	AAGGAATGCACAGTGGAAATATGAATAAATACCGAAACATTTGGTAGTGAACATGGAAG	298
63	LysGluCysThrValGluTyrGluLeuLysTyrArgAsnIleGlySerGluThrTrpLys	82
299	ACCATCATTACTAAGAATCTACATTACAAAGATGGGTTTGATCTTAACAAGGCATTGAA	358
83	ThrIleIleThrLysAsnLeuHisTyrLysAspGlyPheAspLeuAsnLysGlyIleGlu	102
359	GCGAAGATACACACGCTTTTACCATGGCAATGCACAAATGGATCAGAAGTTCAAAGTTCC	418
103	AlaLysIleHisThrLeuLeuProTrpGlnCysThrAsnGlySerGluValGlnSerSer	122
419	TGGGCAGAAACTACTATTGGATATCACCACAAGGAATTCAGAAACTAAAGTTCAGGAT	478
123	TrpAlaGluThrThrTyrTrpIleSerProGlnGlyIleProGluThrLysValGlnAsp	142
479	ATGGATTGCGTATATTACAATTGGCAATATTACTCTGTCTTGGAAACCTGGCATAGGT	538
143	MetAspCysValTyrTyrAsnTrpGlnTyrLeuLeuCysSerTrpLysProGlyIleGly	162
539	GTACTTCTTGATACCAATTACAACCTGTTTTTACTGGTATGAGGCTTGGATCATGCATTA	598
163	ValLeuLeuAspThrAsnTyrAsnLeuPheTyrTrpTyrGluGlyLeuAspHisAlaLeu	182
599	CAGTGTGTGATTACATCAGGCTGATGGACAAATATAGGATGCAGATTTCCCTATTG	658
183	GlnCysValAspTyrIleLysAlaAspGlyGlnAsnIleGlyCysArgPheProTyrLeu	202

FIG.2a

6/19

659	GAGGCATCAGACTATAAGATTTCTATATATTTGTGTTAATGGATCATCAGAGAACAAGCCT	718
203	GluAlaSerAspTyrLysAspPheTyrIleCysValAsnGlySerSerGluAsnLysPro	222
719	ATCAGATCCAGTTATTTCACTTTTCAGCTTCAAAATATAGTTAAACCTTTGCCGCCAGTC	778
223	IleArgSerSerTyrPheThrPheGlnLeuGlnAsnIleValLysProLeuProProVal	242
779	TATCTTACTTTTACTCGGGAGAGTTTCATGTGAAATTAAGCTGAAATGGAGCATACCTTTG	838
243	TyrLeuThrPheThrArgGluSerSerCysGluIleLysLeuLysTrpSerIleProLeu	262
839	GGACCTATTCCAGCAAGGTGTTTGTATTATGAAATTGAGATCAGAGAAGATGATACTACC	898
263	GlyProIleProAlaArgCysPheAspTyrGluIleGluIleArgGluAspThrThr	282
899	TTGGTGACTGCTACAGTTGAAAATGAAACATACACCTTGAAAAACAACAATGAAACCCGA	958
283	LeuValThrAlaThrValGluAsnGluThrTyrThrLeuLysThrThrAsnGluThrArg	302
959	CAATTATGCTTTGTAGTAAGAAGCAAGTGAATATTTATTGCTCAGATGACGGAATTTGG	1018
303	GlnLeuCysPheValValAlaArgSerLysValAsnIleTyrCysSerAspAspGlyIleTrp	322
1019	AGTGAGTGGAGTGATAACAATGCTGGGAAGGTGAAGACCTATCGAAGAAAACTTTGCTA	1078
323	SerGluTrpSerAspLysGlnCysTrpGluGlyGluAspLeuSerLysLysThrLeuLeu	342
1079	CGTTTCTGGCTACCAATTTGGTTTCATCTTAATATATTAGTTATATTTGTAACCGTCTGCTT	1138
343	ArgPheTrpLeuProPheGlyPheIleLeuIleLeuValIlePheValThrGlyLeuLeu	362
1139	TTGCGTAAGCCAAACACCTACCCAAAAATGATTCAGAAATTTTCTGTGATACATGAAGA	1198
363	LeuArgLysProAsnThrTyrProLysMetIleProGluPhePheCysAspThr	381
1199	CTTCCATATCAAGAGACATGGTATTGACTCAACAGTTTCCAGTCATGCCAAATGTTCA	1258
1259	ATATGAGTCTCAATAAACTGAATTTTCTTCCGAATGTTG 1298	

FIG. 2a(continuation)

7/19

IL13R MAFVCLAIGCLYTFLLSTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLY 50
 | | | | | | | |
 IL5R ..MIIVAHVLLILLGATEILLQADLLPDEKISLLPPVNFTIKVTG.LAQVL 47

IL13R LQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKG 100
 | | | | | | | |
 IL5R LQWKPNPDQEQ.RNVNLEYQVKINAPKEDDYETRITES...KCVTILHKG 93

IL13R IEAKIHTLLPWQCTNGSEVQSSWAETTYWISPOGIPETKVQDMDQV.... 146
 | | | | | | | |
 IL5R FSASVRTILQ...NDHSLASSWASAE.LHAPPGSPGTSIVNLTQTTNTT 139

IL13R ..YYNWQ.....YLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIK 189
 | | | | | | | |
 IL5R EDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE..EQEYSK 187

IL13R AD.GONIGORFP..YLEASDYKDFYICVNGSSSENKPIRSSYFTFQLOQIV 236
 | | | | | | | |
 IL5R DTLGRNIAQWFPRTFILSKGRDWLSVLVNGSSKHSAIRPFDQLFALHAID 237

IL13R KPLPPVYLTFRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTA 286
 | | | | | | | |
 IL5R QINPPLNVTAIEIEGT.RLSIQWEKPVSAFPIHCFDYEYVKIHNTNRNGYLQI 286

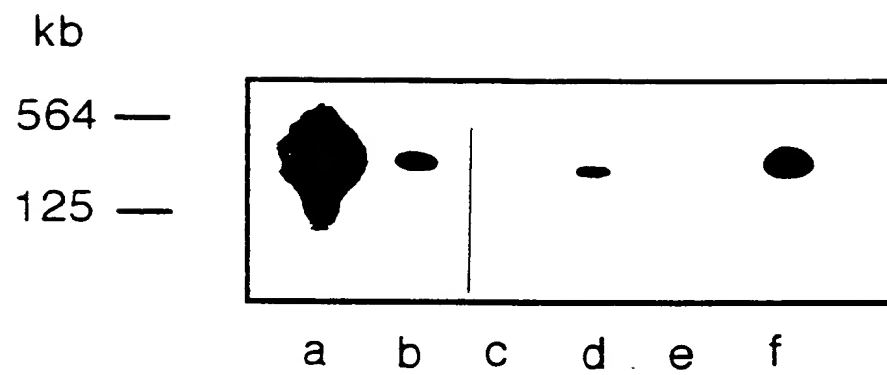
IL13R TVENETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSKQCWEGEDL 336
 | | | | | | | |
 IL5R EKLMTNAFISIIDDLISKYDVQVRAAVSSMCREAGLWSEWSQ.PIYVGND 335

IL13R SKKTLLRFWLPFGFILILVIFVTGLLLRKPNTYPKMIP.....EF 376
 | | | | | | | |
 IL5R HKPLREWFVIVIMATICFILLILSLICKICHLWIKLFPPIPAPKSNIKDL 385

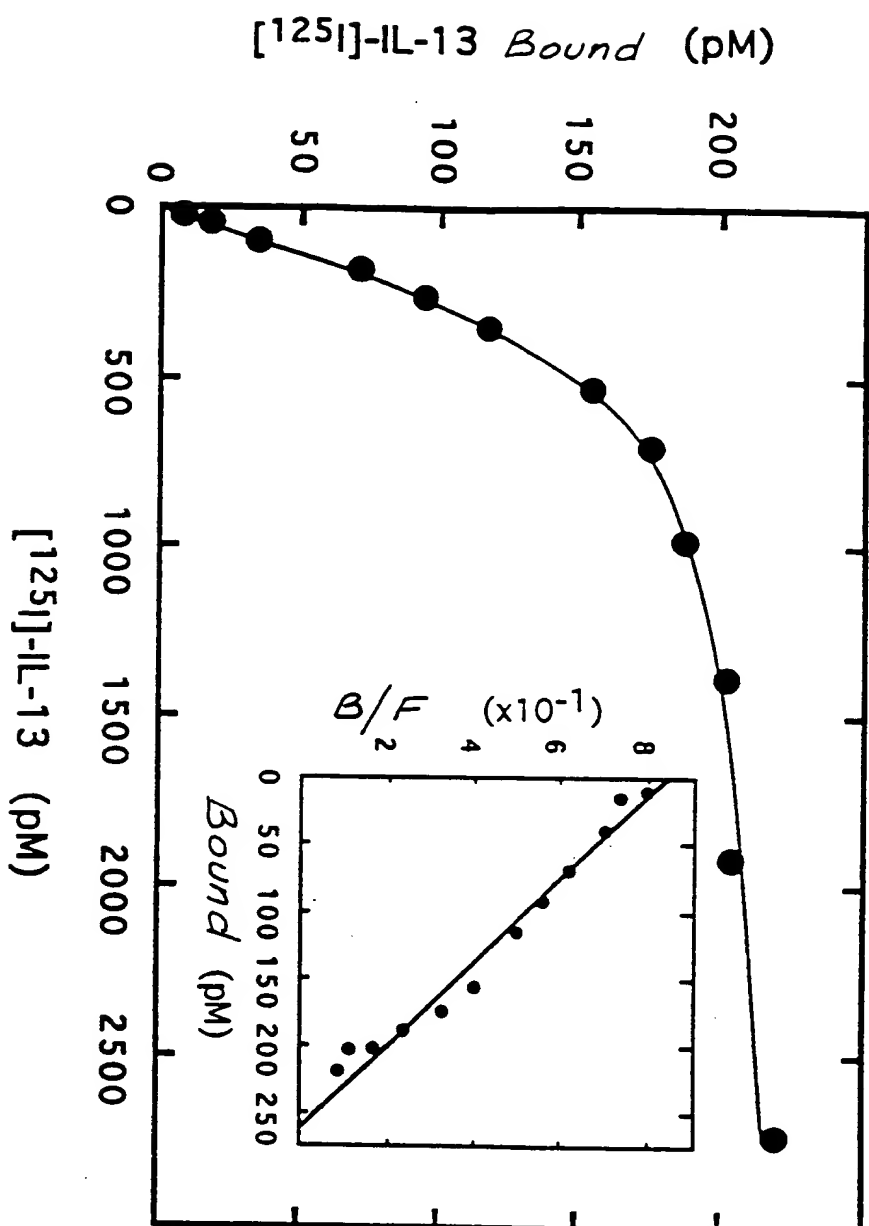
IL13R FCDT..... 380
 |
 IL5R FVTTNYEKAGSSETEIEVICYIEKPGVETLEDSVF 420

FIG. 2b

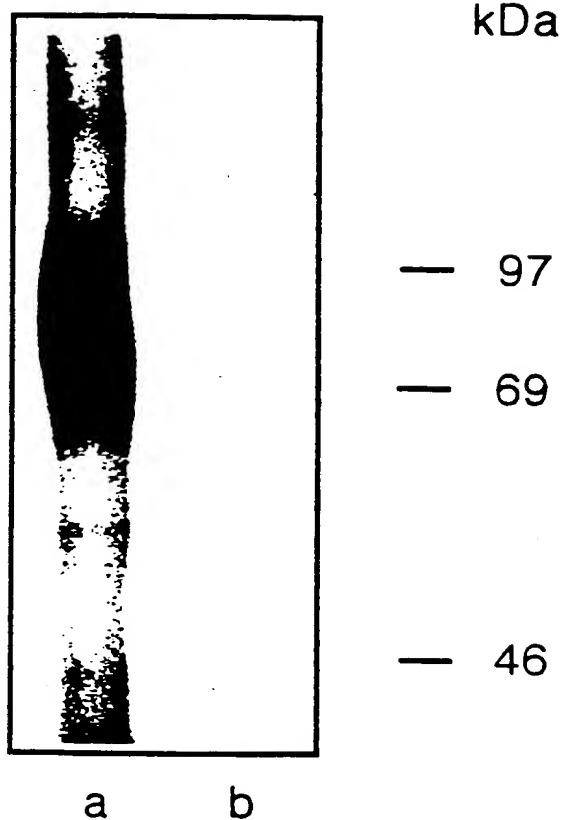
8/19

FIG.3

9/19

FIG. 4a

10/19

FIG.4b

11/19

09077817-091498

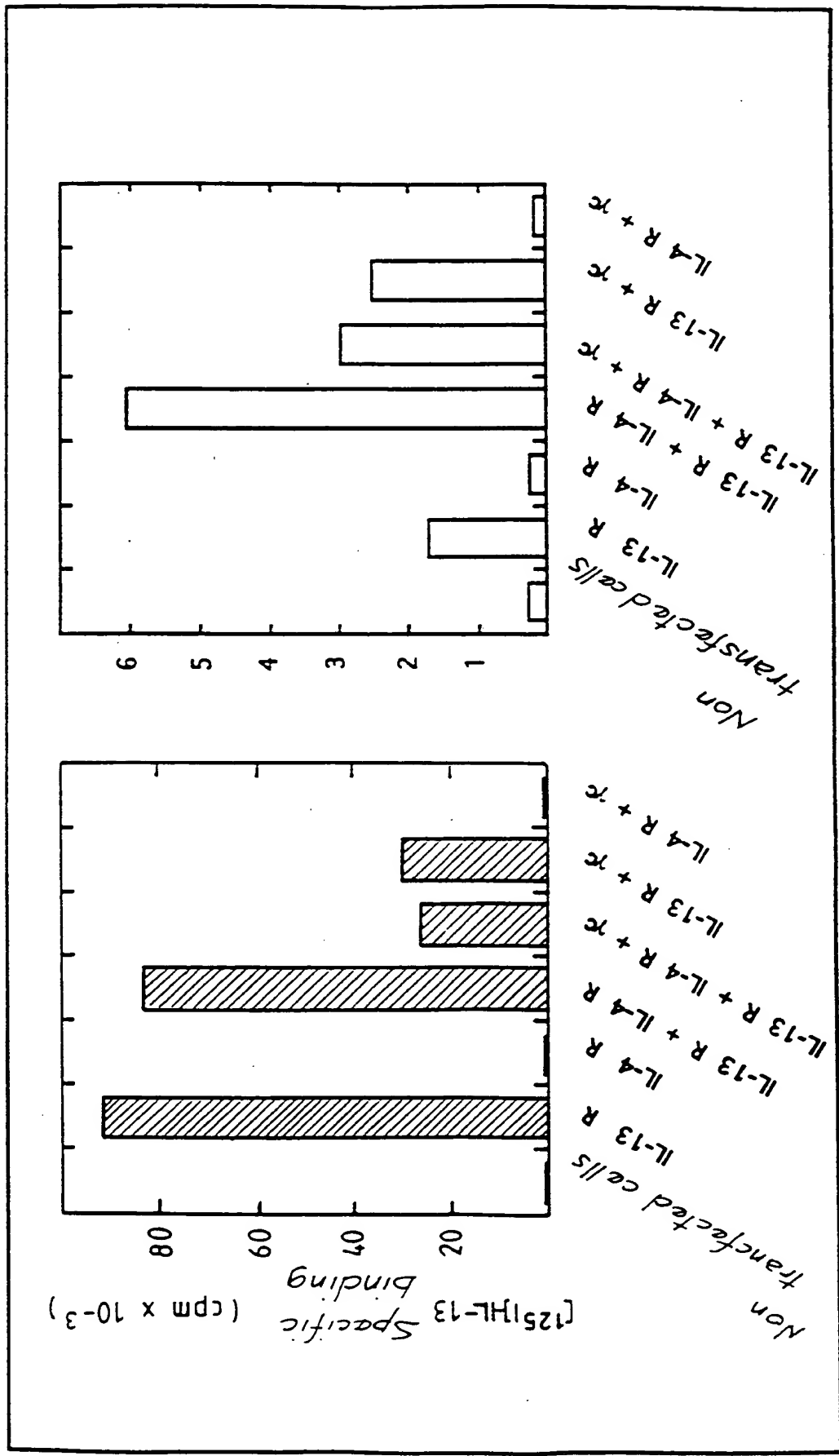


FIG. 4C

12/19

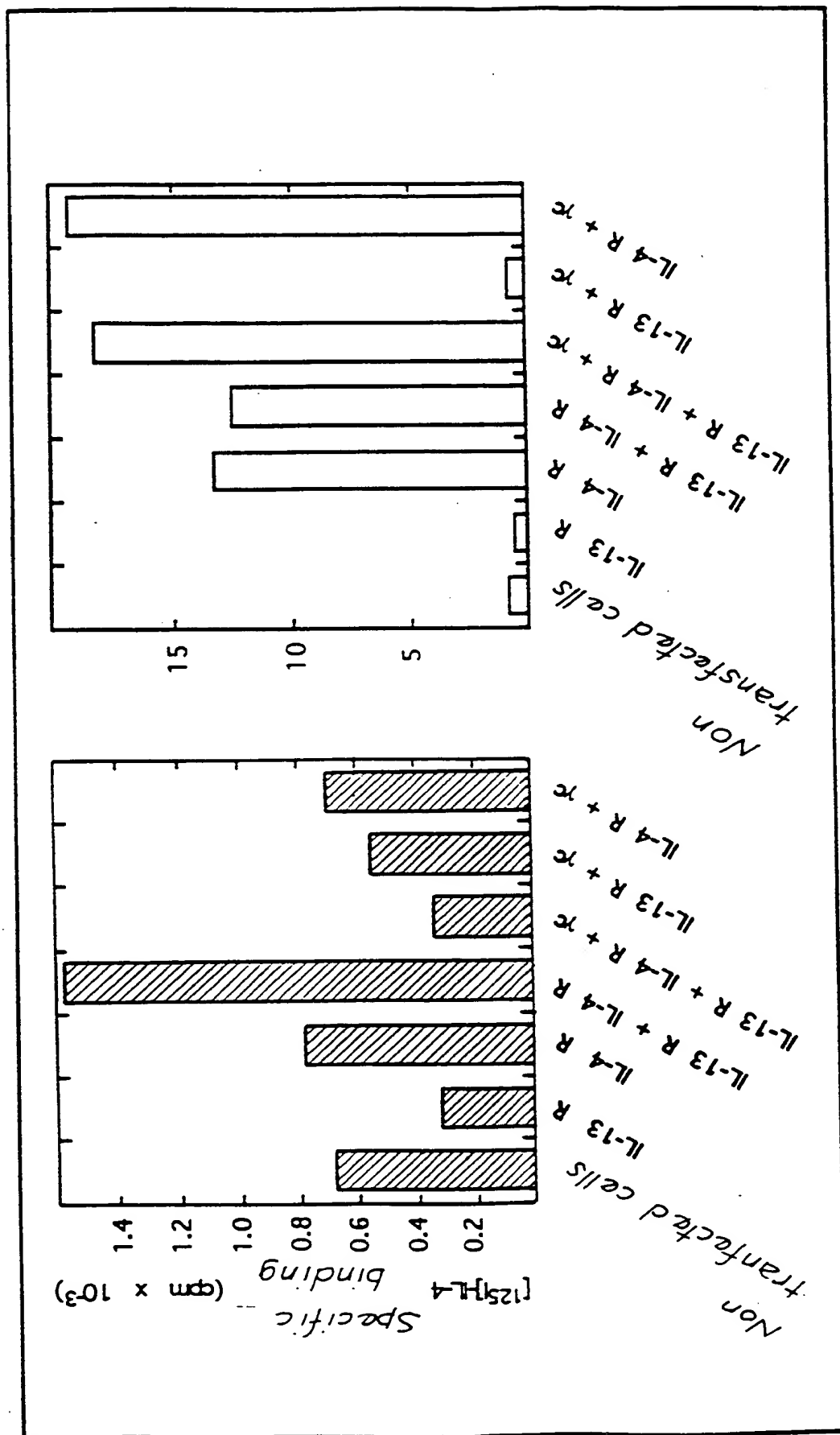


FIG. 4d

13/19

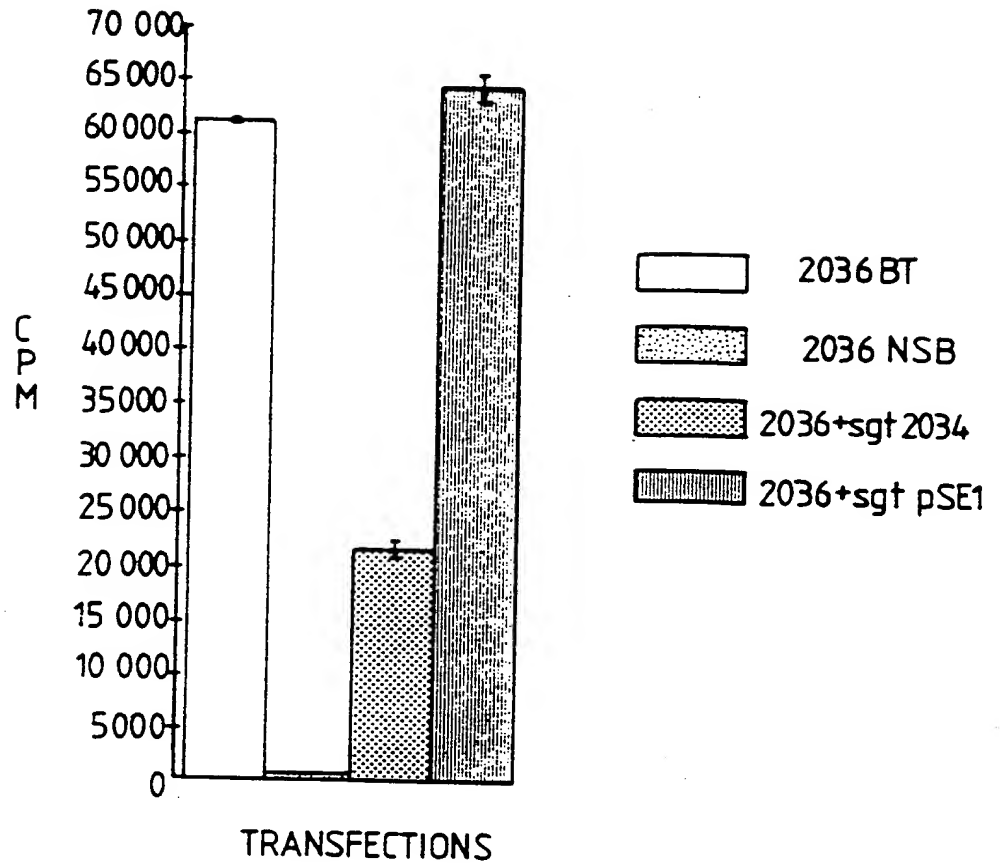
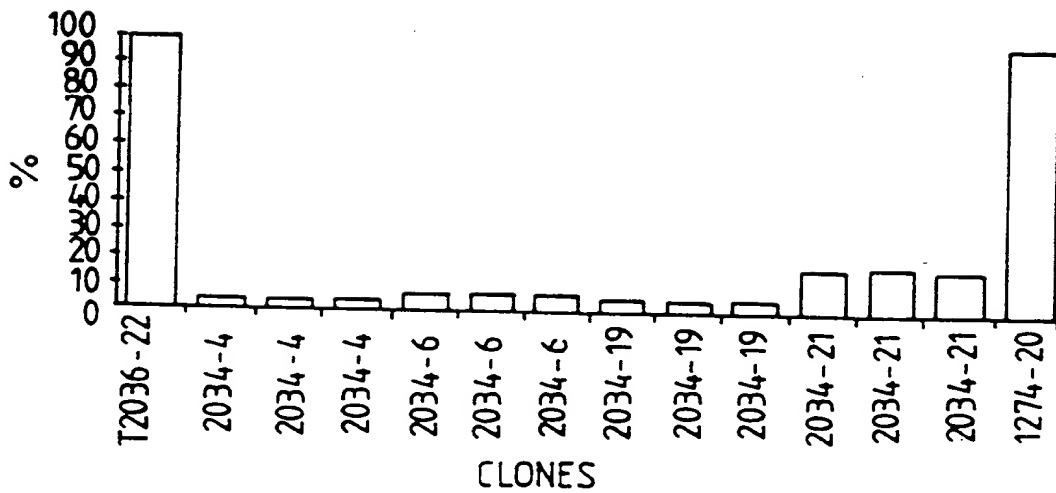


FIG. 5

FIG. 6



14/19

1 TCAGCCCGGCCGGGCTCCGAGGCGAGAGGCTGCATGGAGTGGCCGGCGCGGCTCTGCGGG 60
 -10 M E W P A R L C G 9
 61 CTGTGGGCGCTGCTGCTCTGCGCCGGCGGGGGCGGGGGCGCGCGCTACG 120
 10 L W A L L L C A G G G G G G A A P T 29
 121 GAAACTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATA 180
 30 E T Q P P V T [N L S V] S V E N L C T V I 49
 181 TGGACATGGAATCCACCCGAGGGAGCCAGCTCAAATTGTAGTCTATGGTATTTTAGTCAT 240
 50 W T W N P P E G A S S [N C S L] W Y F S H 69
 241 TTTGGCGACAAACAAGATAAGAAAATAGCTCCGGAAACTCGTCGTTCAATAGAAGTACCC 300
 70 F G D K Q D K K I A P E T R R S I E V P 89
 301 CcGAATGAGAGGATTTGTCTGCAAGTGGGGTCCAGTGATGACCAATGAGAGTGAGAAG 360
 90 L N E R I C L Q V G S Q C S T [N E S E] K 109
 361 CCTAGCATTTTGGTTGAAAAATGCATCTCACCCCGAGAAGGTGATCCTGAGTCTGCTGTG 420
 110 P S I L V E K C I S P P E G D P E S A V 129
 421 ACTGAGCTTCAATGCATTTGGCACAACCTGAGCTACATGAAGTGTTCTTGGCTCCCTGGA 480
 130 T E L Q C I W H [N L S Y] M K C S W L P G 149
 481 AGGAATACCAGTCCCGACACTAACTATACTCTCTACTATTGGCACAGAAGCCTGGAAAAA 540
 150 R N T S P D T [N Y T L] Y Y W H R S L E K 169
 541 ATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATACTTTGGTTGTTCTTTGATCTG 600
 170 I H Q C E N I F R E G Q Y F G C S F D L 189
 601 ACCAAAGTGAAGGATTCCAGTTTTGAACAACACAGTGTCCAAATAATGGTCAAGGATAAT 660
 190 T K V K D S S F E Q H S V Q I M V K D N 209
 661 GCAGGAAAAATTAAACCATCCTTCAATATAGTGCCTTTAACTTCCCGTGTGAAACCTGAT 720
 210 A G K I K P S F N I V P L T S R V K P D 229
 721 CCTCCACATATTA AAAACCTCTCCTTCCACAATGATGACCTATATGTGCAATGGGAGAAT 780
 230 P P H I K [N L S F] H N D D L Y V Q W E N 249
 781 CCACAGAATTTTATTAGCAGATGCCTATTTTATGAAGTAGAAGTCAATAACAGCCAACT 840
 250 P Q N F I S R C L F Y E V E V [N N S Q] T 269
 841 GAGACACATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAATCCAGAATTTGAGAGA 900
 270 E T H N V F Y V Q E A K C E N P E F E R 289
 901 AATGTGGAGAATACATCTTGTTCATGGTCCCTGGTGTCTTCTCTGATACTTTGAACACA 960
 290 N V E [N T S C] F M V P G V L P D T L N T 309
 961 GTCAGAATAAGAGTCAAAACAAATAAGTTATGCTATGAGGATGACAAACTCTGGAGTAAT 1020
 310 V R I R V K T N K L C Y E D D K L W S [N] 329
 1021 TGGAGCCAAGAAATGAGTATAGGTAAGAAGCGCAATTCCACACTCTACATAACCATGTTA 1080
 330 [W S Q] E M S I G K K R [N S T L] Y I T M L 349
 1081 CTCATTGTTCCAGTCATCGTCGAGGTGCAATCATAGTACTCCTGCTTTACCTAAAAAGG 1140
 350 L I V P V I V A G A I I V L L L Y L K R 369
 1141 CTCAAGATTATTATATTCCTCCAATTCTGATCCTGGCAAGATTTTAAAGAAATGTTT 1200
 370 L K I I I F P P I P D P G K I F K E M F 389
 1201 GGAGACCAGAATGATGATACTCTGCACTGGAAGAAGTACGACATCTATGAGAAGCAAACC 1260
 390 G D Q N D D T L H W K K Y D I Y E K Q T 409
 1261 AAGGAGGAAACCGACTCTGTAGTGCTGATAGAAAACCTGAAGAAAGCCTCTCAGTGATGG 1320
 410 K E E T D S V V L I E N L K K A S Q * 429

FIG.7a

09077817-094496

15/19

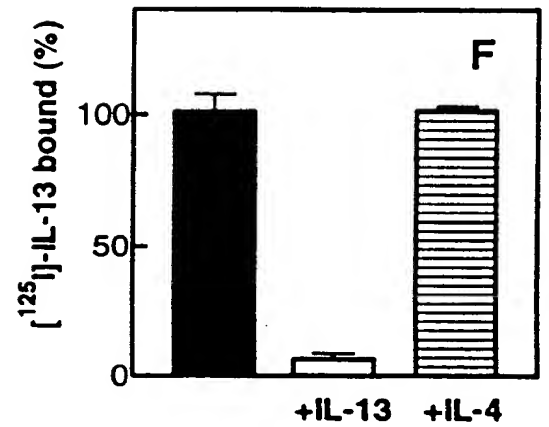
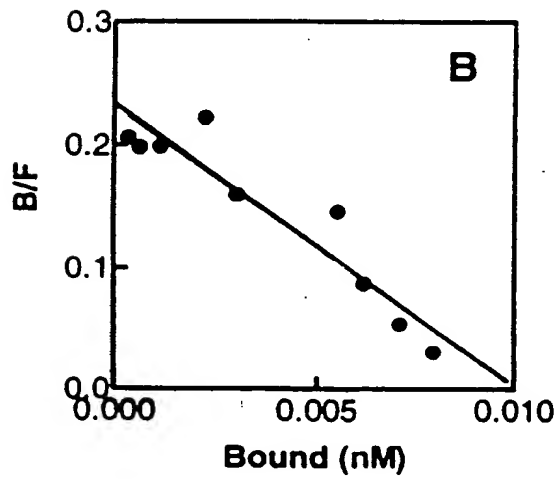
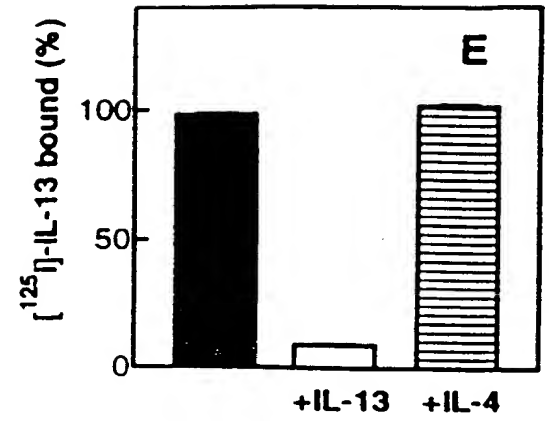
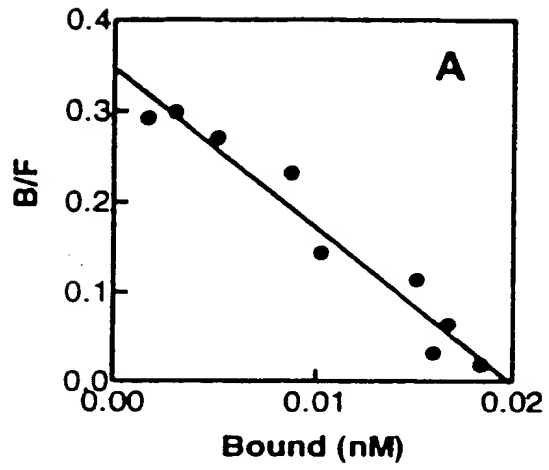
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 1441 ATAAGAGCCACAGGTCCTTATGTTGAGTCGCGCACCCGAAAAACTAAAAATAATGGGCGCT 1500
 1501 TTGGAGAAGAGTGTGGAGTCATTCTCATTGAATTATAAAAGCCAGCAGGCTTCAAACCTAG 1560
 1561 GGGACAAAGCAAAAAGTGATGATAGTGGTGGAGTTAATCTTATCAAGAGTTGTGACAACCT 1620
 1621 TCCTGAGGGATCTATACTTGCTTTGTGTTCTTTGTGTCAACATGAACAAATTTTATTTGT 1680
 1681 AGGGGAACTCATTGTTGGGTGCAAATGCTAATGTCAAACCTGAGTCACAAAGAACATGTAG 1740
 1741 AAAACAAAATGGATAAAATCTGATATGTATTGTTGGGATCCTATTGAACCATGTTTGTG 1800
 1801 GCTATTAAAACTCTTTTAACAGTCTGGGCTGGGTCCGGTGGCTCACGCCGTGTAATCCCAG 1860
 1861 CAATTTGGGAGTCCGAGGCGGGCGGATCACTCGAGGTCAGGAGTTCCAGACCAGCCTGAC 1920
 1921 CAAAATGGTGAAACCTCCTCTCTACTAAAACCTACAAAAATTAAGTGGGTGTGGTGGCGCG 1980
 1981 TGCCTGTAATCCCAGCTACTCGGGAAGCTGAGGCAGGTGAATTGTTTGAACCTGGGAGGT 2040
 2041 GGAGGTTGCAGTGAGCAGAGATCACACCACTGCCTCTAGCCTGGGTGACAGAGCAAGAC 2100
 2101 TCTGTCTAAAAAACAAAACAAAACAAAACAAAACAAAACCTCTTAATATTCTGGAGT 2160
 2161 CATCATTCCTCTCGACAGCATTTTCTCTGCTTTTGAAGGCCCCAGAAATCAGTGTGTGGCC 2220
 2221 ATGATGACAACCTACAGAAAAACCAGAGGCAGCTTCTTTGCCAAGACCTTTCAAAGCCATT 2280
 2281 TTAGGCTGTTAGGGGCAGTGGAGGTAGTAACTGCTCTTGGGTATTAGAGTTTCAACCATG 2340
 2341 AAGTCTCTAACAATGTATTTCTTACCTCTGCTACTCAAGTAGCATTTACTGTGTCTTT 2400
 2401 GGTTTGTGCTAGGCCCCCGGGTGTGAAGCACAGACCCCTTCCAGGGGTTTACAGTCTAT 2460
 2461 TGAGACTCCTCAGTTCTTGCCACTTTTTTTTTTAATCTCCACCAGTCATTTTTTCAGACCT 2520
 2521 TTTAACTCCTCAATTTCCAACACTGATTTCCCTTTTGCATTCTCCCTCCTTCCCTTCCCT 2580
 2581 GTAGCCTTTTGACTTTTCAATTGGAAATTAGGATGTAAATCTGCTCAGGAGACCTGGAGGAG 2640
 2641 CAGAGGATAATTAGCATCTCAGGTAAAGTGTGAGTAATCTGAGAAACAATGACTAATTCT 2700
 2701 TGCATATTTTGTAACTTCCATGTGAGGGTTTTTCAGCATTGATATTTGTGCATTTTCTAAA 2760
 2761 CAGAGATGAGGTGGTATCTTACGTTAGAACATTGGTATTGCTTGGAGAAAAAAGAATAG 2820
 2821 TTGAACCTATTTCTCTTTCTTTACAAGATGGGTCCAGGATTCCTCTTTTCTCTGCCATAA 2880
 2881 ATGATTAATTAAATAGCTTTTGTGTCTTACATTGGTAGCCAGCCAGCCAAGGCTCTGTTT 2940
 2941 ATGCTTTTGGGGGGCATATATTGGGTTCATTCTCACCTATCCACACAACATATCCGTAT 3000
 3001 ATATCCCCTCTACTCTTACTTCCCCCAAATTTAAAGAAGTATGGGAAATGAGAGGCATTT 3060
 3061 CCCCCACCCCATTTCTCTCCTCACACACAGACTCATATTACTGGTAGGAACCTTGAGAACT 3120
 3121 TTATTTCCAAGTTGTTCAAACATTTACCAATCATATTAATACAATGATGCTATTTGCAAT 3180
 3181 TCCTGCTCCTAGGGGAGGGGAGATAAGAAACCCTCACTCTCTACAGGTTTGGGTACAAGT 3240
 3241 GGCAACCTGCTTCCATGGCCGTGTAGAAGCATGGTGCCCTGGCTTCTCTGAGGAAGCTGG 3300
 3301 GGTTTCATGACAATGGCAGATGTAAAGTTATTCTTGAAGTCAGATTGAGGCTGGGAGACAG 3360
 3361 CCGTAGTAGATGTTCTACTTTGTCTGCTGTTCTCTAGAAAGAATATTTGGTTTTCTGT 3420
 3421 ATAGGAATGAGATTAATTCCTTTCCAGGTATTTTATAATTCTGGGAAGCAAAACCCATGC 3480
 3481 CTCCCCCTAGCCATTTTTACTGTTATCCTATTTAGATGGCCATGAAGAGGATGCTGTGAA 3540
 3541 ATTCCCAACAAACATTGATGCTGACAGTCATGCAGTCTGGGAGTGGGGAAGTGATCTTTT 3600
 3601 GTTCCCATCCTCTCTTTTAGCAGTAAAATAGCTGAGGGAAGGGAGGGAAGGAAGT 3660
 3661 TATGGGAATACCTGTGGTGGTTGTGATCCCTAGGTCTTGGGAGCTCTTGGAGGTGTCTGT 3720
 3721 ATCAGTGGATTTCCCATCCCTGTGGGAAATTAGTAGGCTCATTTACTGTTTTAGGTCTA 3780
 3781 GCCTATGTGGATTTTTCTTAACATACCTAAGCAAACCCAGTGTGAGGATGGTAATCTT 3840
 3841 ATTCTTTCGTTTCAGTTAAGTTTTTCCCTTCATCTGGGCACTGAAGGGATATGTGAAACAA 3900
 3901 TGTTAACATTTTTGGTAGTCTTCAACCAGGGATTGTTTCTGTTTAACTTCTTATAGGAAA 3960
 3961 GCTTGAGTAAAAATAAATATTGTCTTTTTGTATGTCACCCAAAAAaaaaa 4009

FIG. 7a(continuation)

IL-13 α MOUSE

FIG. 7b

17/19

FIG. 8

18/19

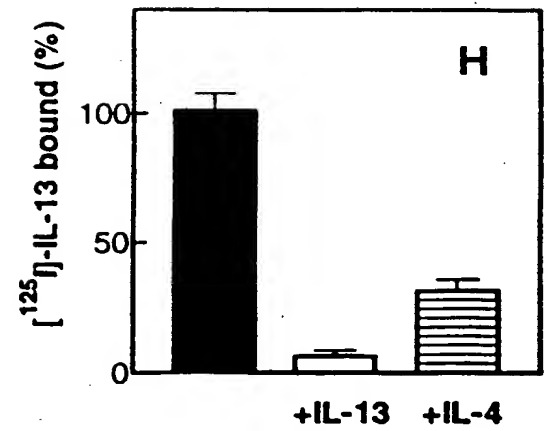
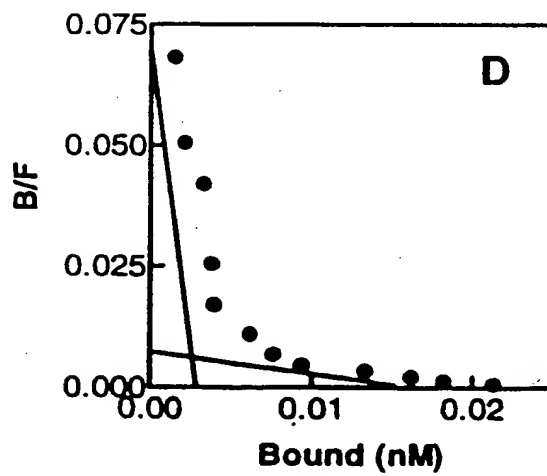
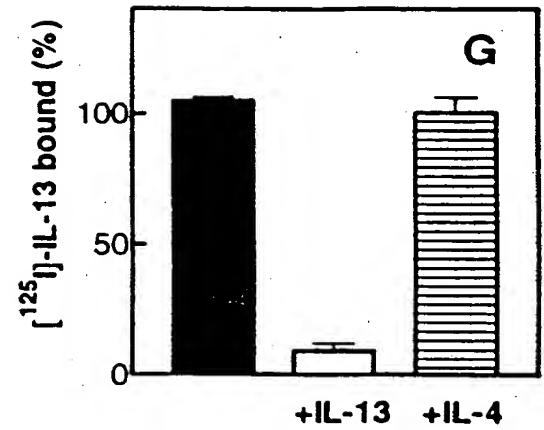
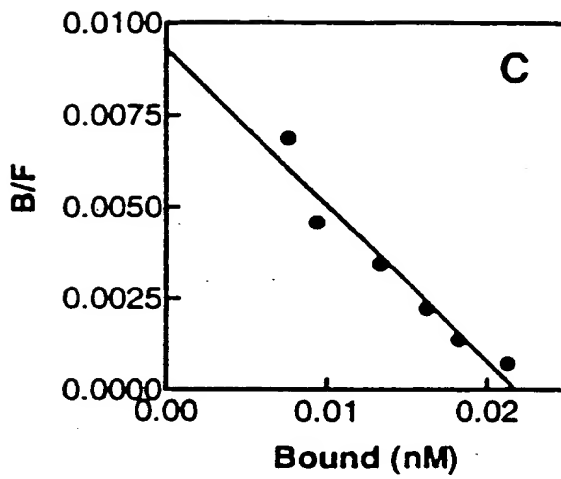
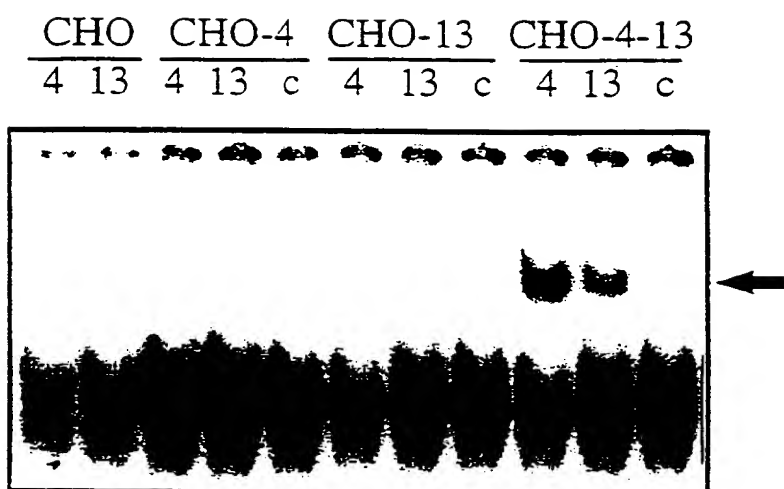


FIG. 8 (continuation)

19/19

FIG.9